

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2017/08/09 15:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/bethany/projects/planctomycetes+halococci/QC/Gem_JW11.sorted.ba
m -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	blasr /home/bethany/projects/planctomycet es/pacbio_raw/Jw11/Analysis_Result s/m170310_123937_42242_c101145 002550000001823272107071731_s1 _p0.bas.h5 /home/bethany/projects/planctomycet es/assembly/final_contigs/Gem_JW1 1_final_contigs.fasta --sam --nproc 16 --out Gem_JW11.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	1 (5.3.574e1c2)
Analysis date:	Wed Aug 09 15:09:45 NZST 2017
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/bethany/projects/planctomycet es+halococci/QC/Gem_JW11.sorted. bam

2. Summary

2.1. Globals

Reference size	8,846,881
Number of reads	184,384
Mapped reads	184,384 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	44 / 42,886 / 9,718.38
Duplicated reads (estimated)	38,053 / 20.64%
Duplication rate	8.94%
Clipped reads	184,375 / 100%

2.2. ACGT Content

Number/percentage of A's	121,151,332 / 16%
Number/percentage of C's	250,242,080 / 33.04%
Number/percentage of T's	120,667,543 / 15.93%
Number/percentage of G's	250,611,569 / 33.09%
Number/percentage of N's	0 / 0%
GC Percentage	66.13%

2.3. Coverage

Mean	90.7284
Standard Deviation	31.5229

2.4. Mapping Quality

Mean Mapping Quality	228
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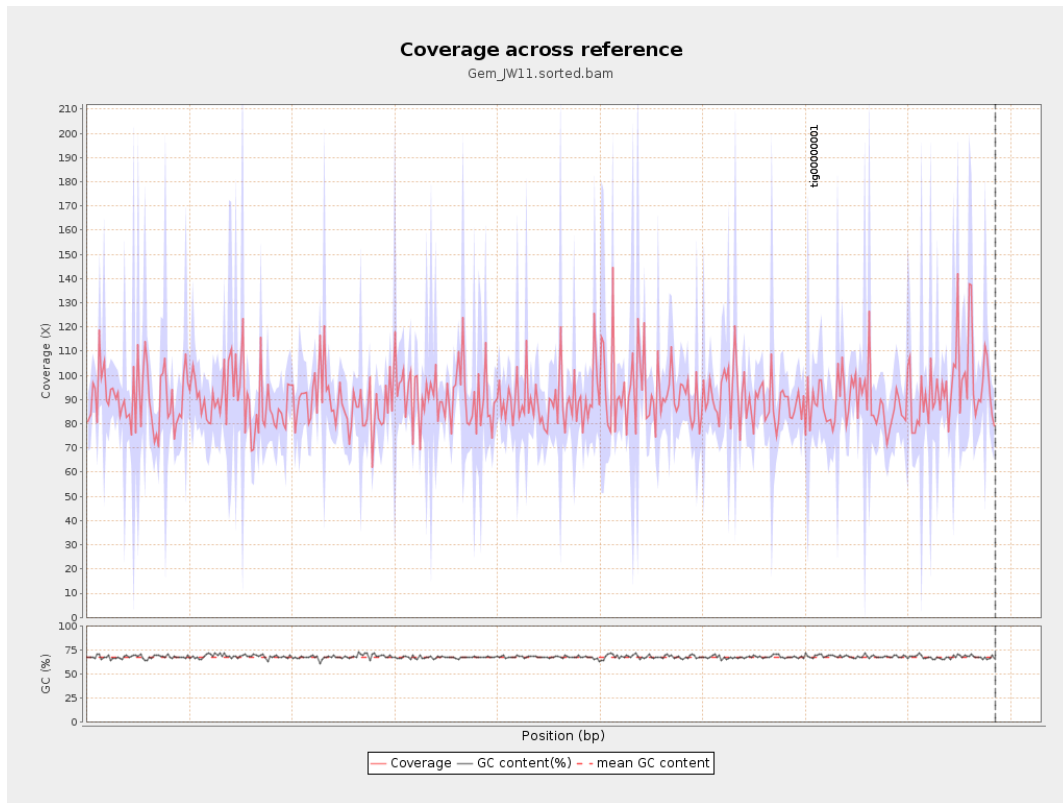
2.5. Mismatches and indels

General error rate	15.97%
Insertions	50,683,158
Mapped reads with at least one insertion	99.33%
Deletions	40,705,289
Mapped reads with at least one deletion	98.92%
Homopolymer indels	20.52%

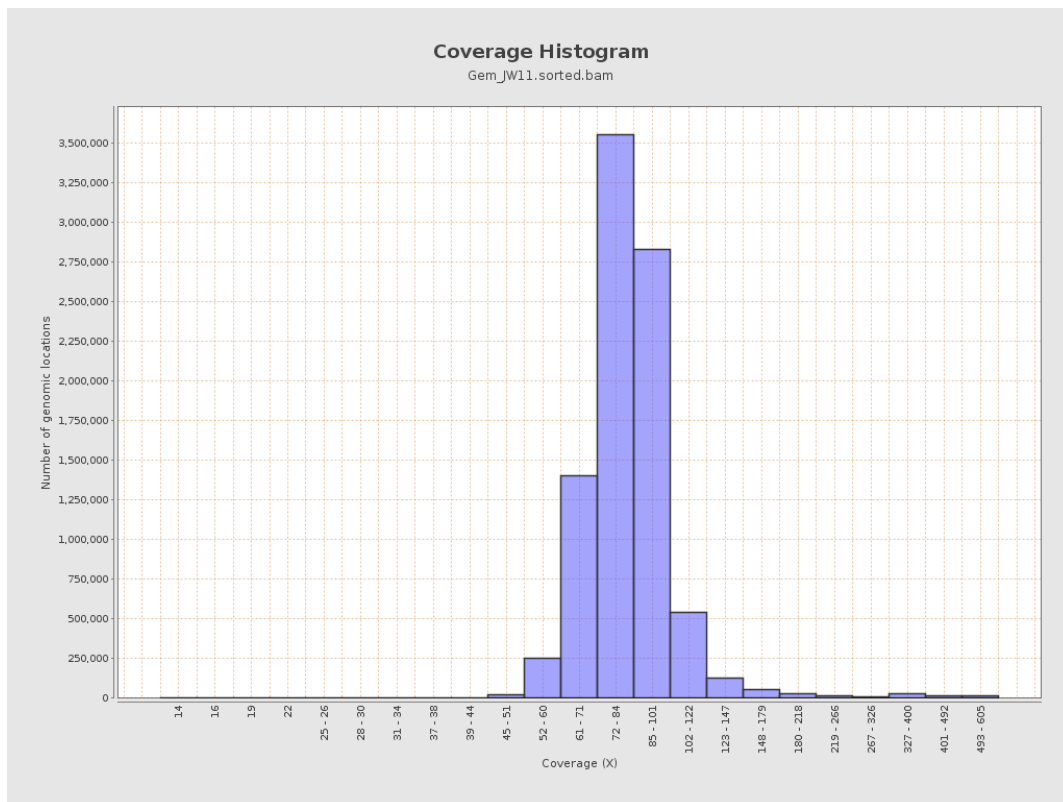
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
tig00000001	8846881	802663540	90.7284	31.5229

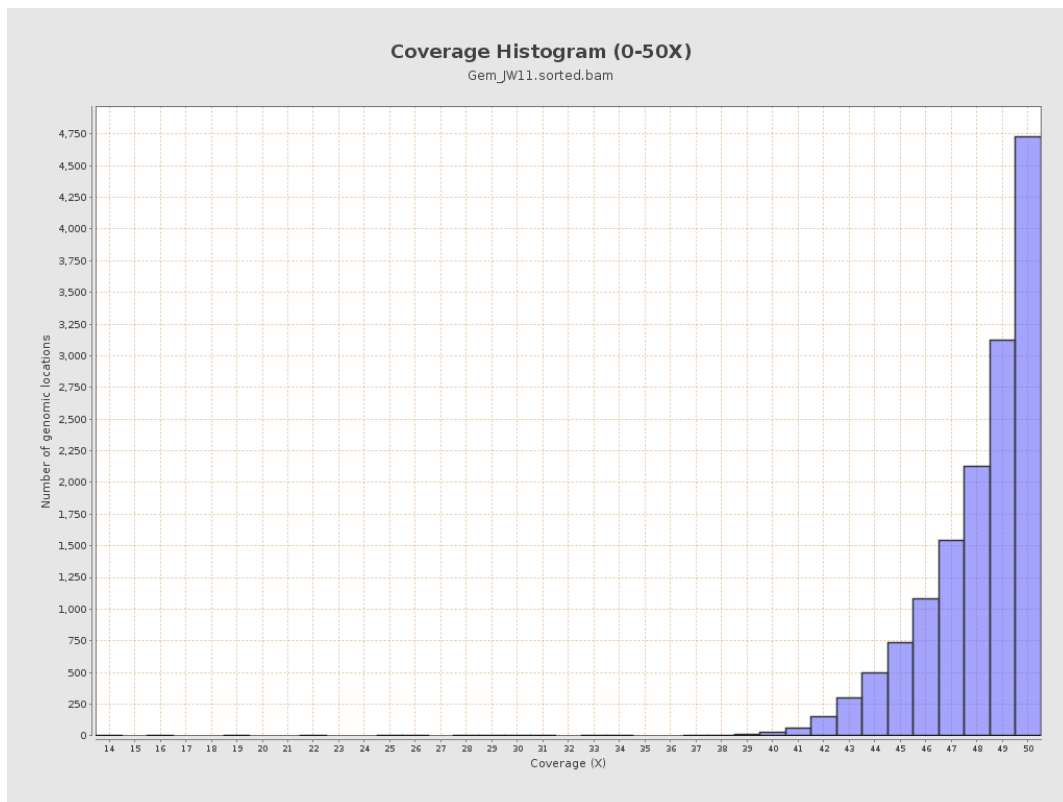
3. Results : Coverage across reference



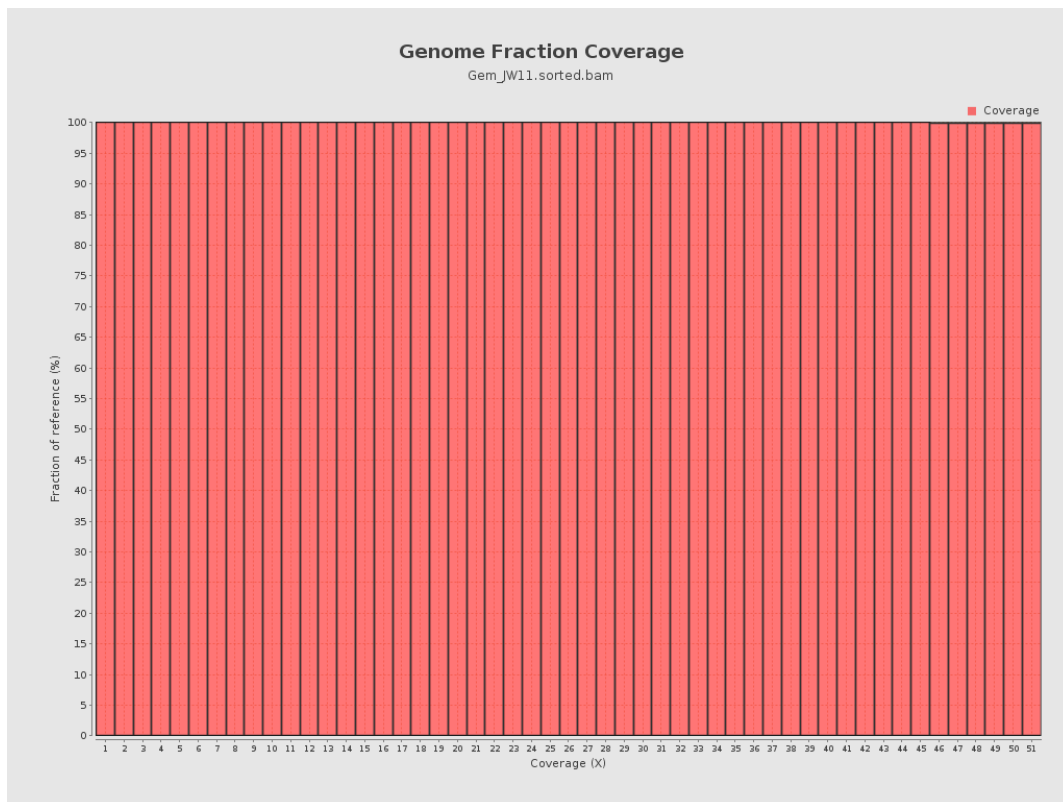
4. Results : Coverage Histogram



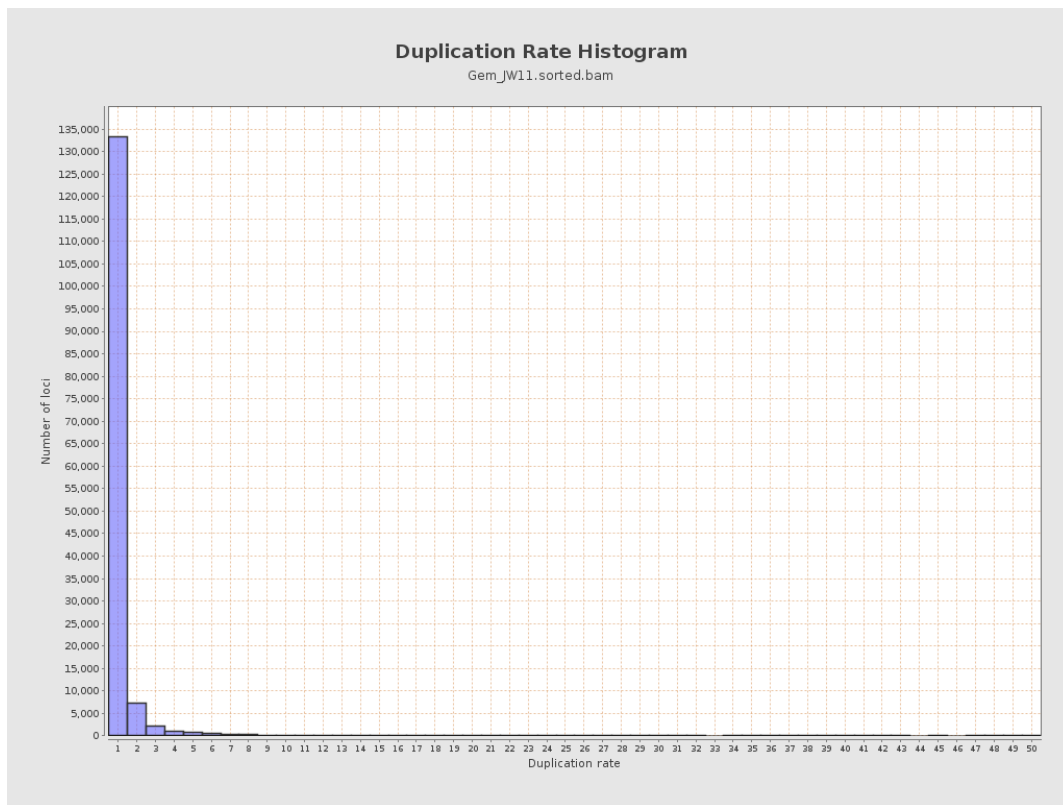
5. Results : Coverage Histogram (0-50X)



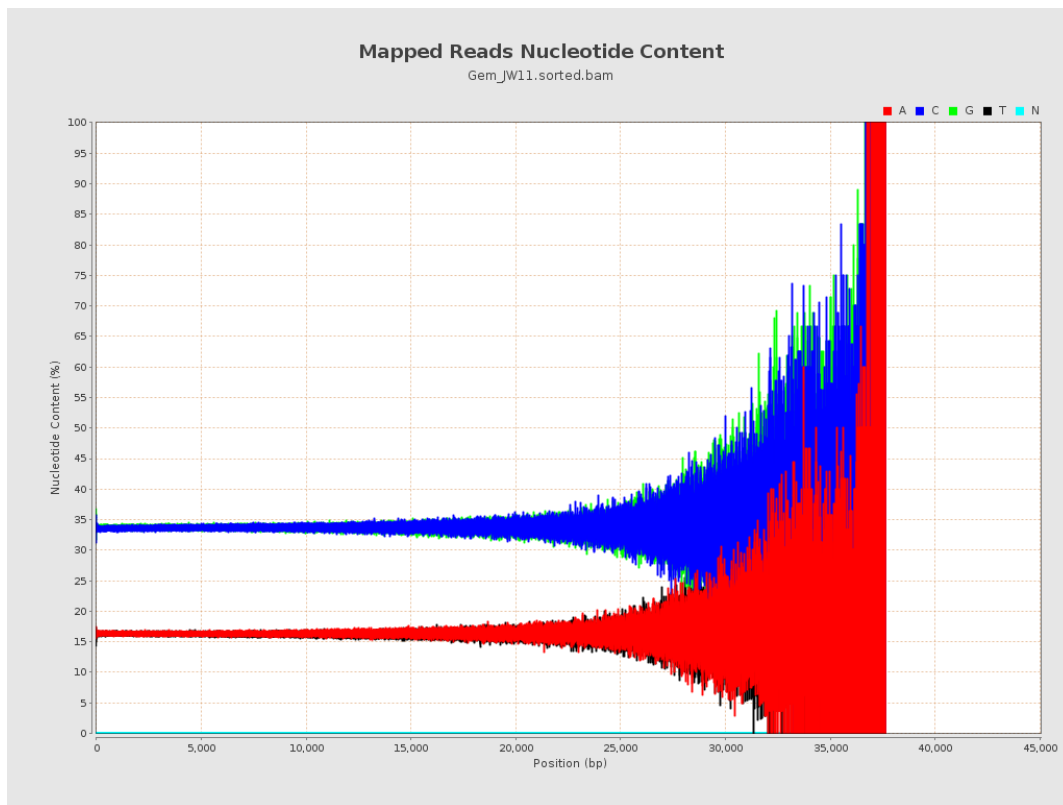
6. Results : Genome Fraction Coverage



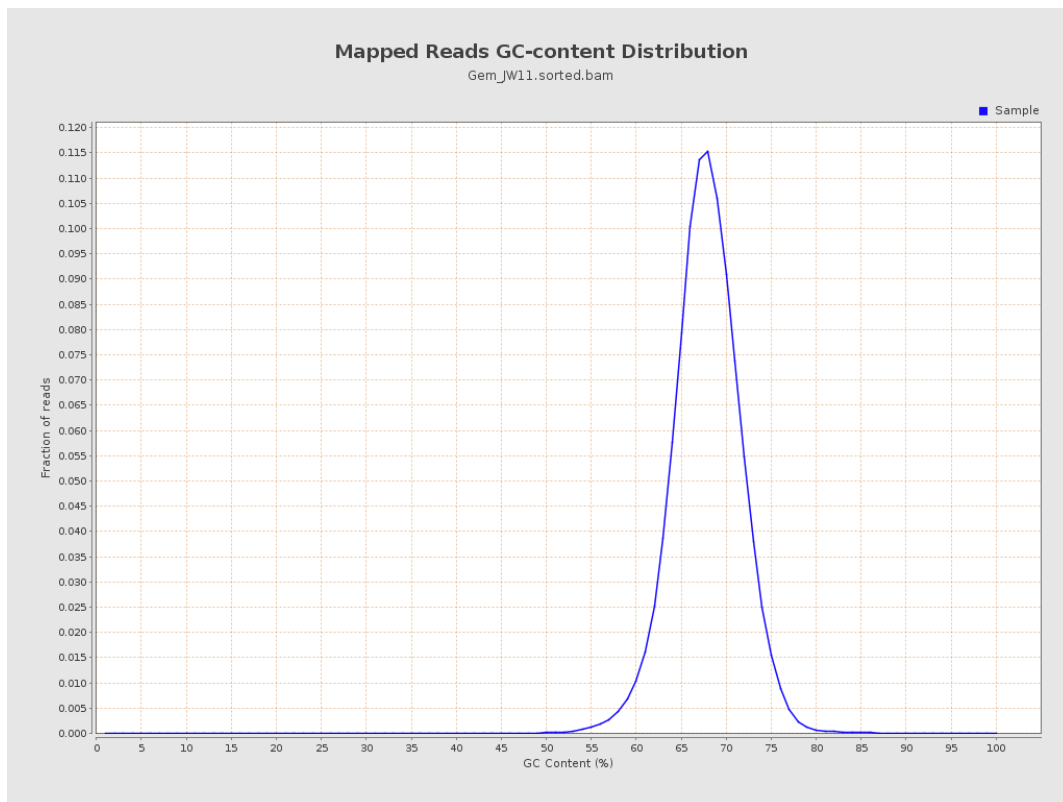
7. Results : Duplication Rate Histogram



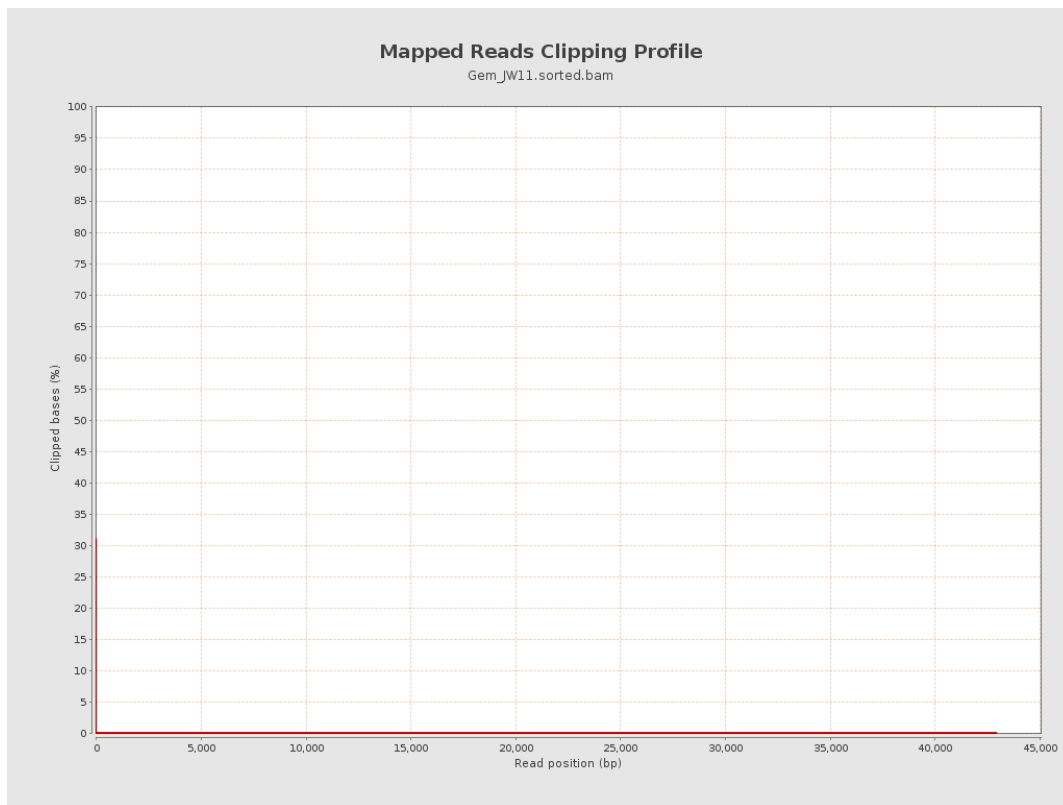
8. Results : Mapped Reads Nucleotide Content



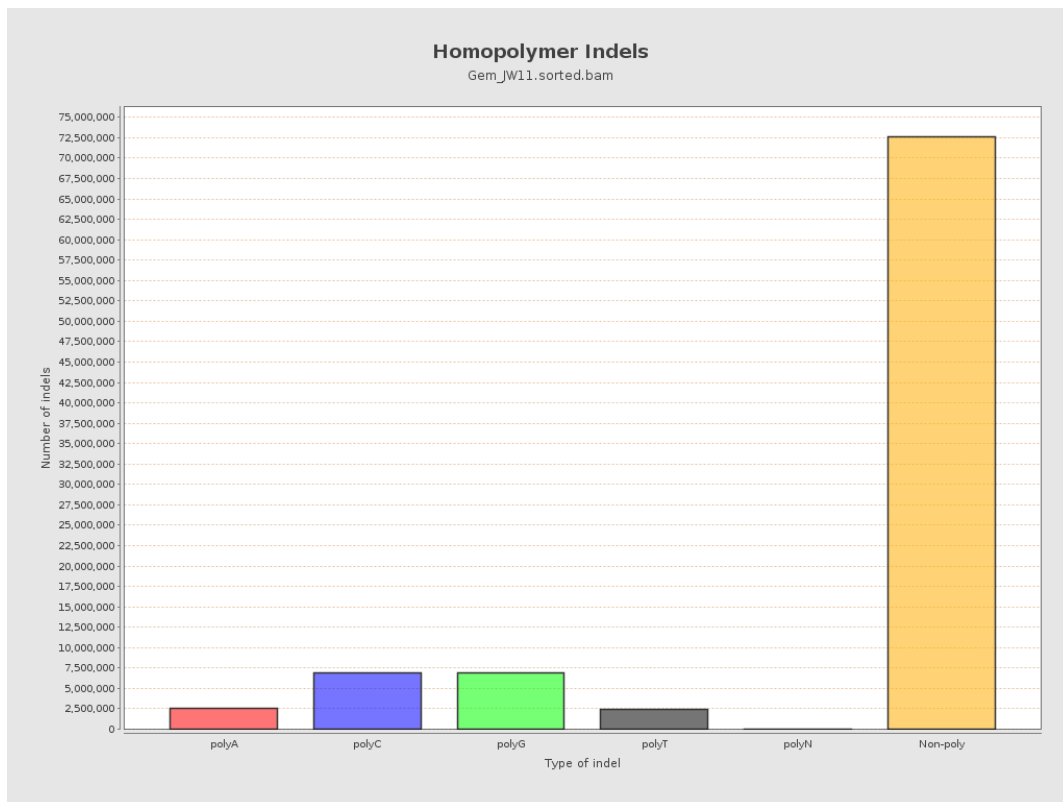
9. Results : Mapped Reads GC-content Distribution



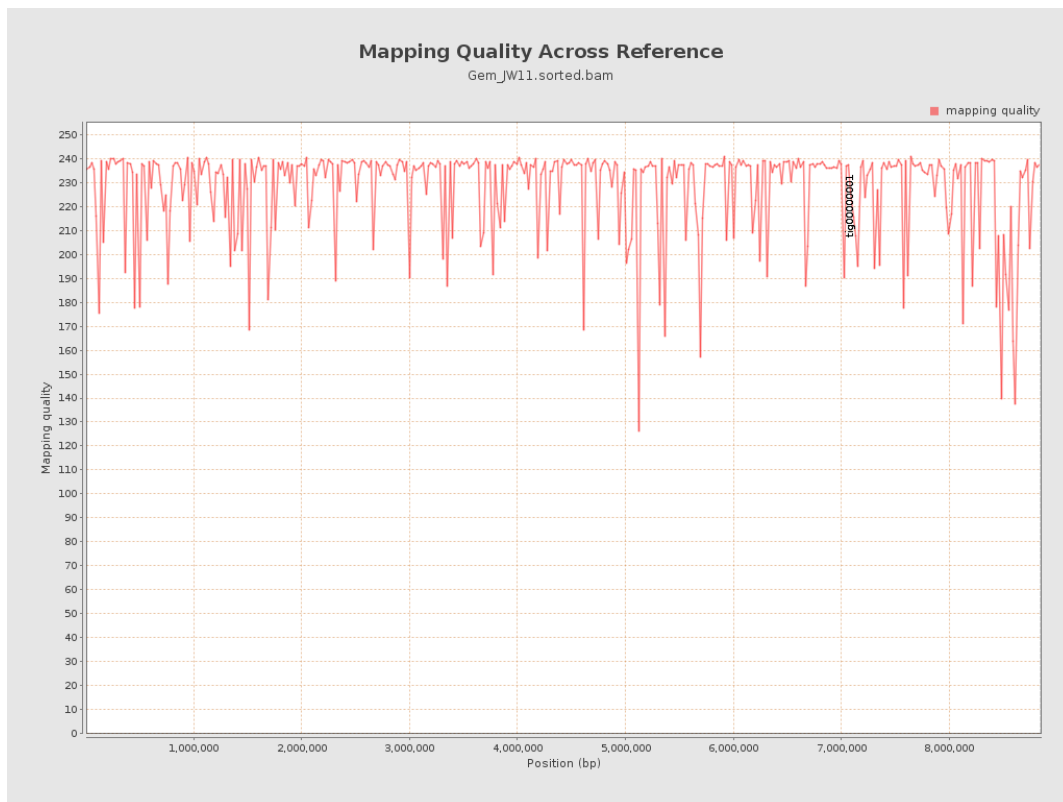
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

